SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana
Millennium Pharmaceuticals, Inc.

<120> 14171 Protein Kinase, A Novel Human Protein Kinase and Uses Thereof

<130> MPI00-010P1RCP1M

<150> 09/781,882
<151> 2001-02-12

<150> 60/182,096
<151> 2000-02-11

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ctg ctg cgc acc ttc gac gcg ggc gag ttc acg ggc tgg gag aag gtg      100
Leu Leu Arg Thr Phe Asp Ala Gly Glu Phe Thr Gly Trp Glu Lys Val
         15                  20                  25

ggc tcg ggc ggc ttc ggg cag gtg tac aag gtg cgc cat gtc cac tgg      148
Gly Ser Gly Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp
     30                  35                  40

aag acc tgg ctg gcc atc aag tgc tcg ccc agc ctg cac gtc gac gac      196
Lys Thr Trp Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp
 45                  50                  55                  60

agg gag cgc atg gag ctt ttg gaa gaa gcc aag aag atg gag atg gcc      244
Arg Glu Arg Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala
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aag ttt cgc tac atc ctg cct gtg tat ggc atc tgc cgc gaa cct gtc      292
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Lys Phe Arg Tyr Ile Leu Pro Val Tyr Gly Ile Cys Arg Glu Pro Val
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ggc ctg gtc atg gag tac atg gag acg ggc tcc ctg gaa aag ctg ctg      340
Gly Leu Val Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu
        95                  100                 105

gct tcg gag cca ttg cca tgg gat ctc cgg ttc cga atc atc cac gag      388
Ala Ser Glu Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Ile His Glu
    110                 115                 120

acg gcg gtg ggc atg aac ttc ctg cac tgc atg gcc ccg cca ctc ctg      436
Thr Ala Val Gly Met Asn Phe Leu His Cys Met Ala Pro Pro Leu Leu
125                 130                 135                 140

cac ctg gac ctc aag ccc gcg aac atc ctg ctg gat gcc cac tac cac      484
His Leu Asp Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His
                145                 150                 155

gtc aag att tct gat ttt ggt ctg gcc aag tgc aac ggg ctg tcc cac      532
Val Lys Ile Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Leu Ser His
            160                 165                 170

tcg cat gac ctc agc atg gat ggc ctg ttt ggc aca atc gcc tac ctc      580
Ser His Asp Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu
        175                 180                 185

cct cca gag cgc atc agg gag aag agc cgg ctc ttc gac acc aag cac      628
Pro Pro Glu Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His
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gat gta tac agc ttt gcg atc gtc atc tgg ggc gtg ctc aca cag aag      676
Asp Val Tyr Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys
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aag ccg ttt gca gat gag aag aac atc ctg cac atc atg gtg aag gtg      724
Lys Pro Phe Ala Asp Glu Lys Asn Ile Leu His Ile Met Val Lys Val
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gtg aag ggc cac cgc ccc gag ctg ccg ccc gtg tgc aga gcc cgg ccg      772
Val Lys Gly His Arg Pro Glu Leu Pro Pro Val Cys Arg Ala Arg Pro
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cgc gcc tgc agc cac ctg ata cgc ctc atg cag cgg tgc tgg cag ggg      820
Arg Ala Cys Ser His Leu Ile Arg Leu Met Gln Arg Cys Trp Gln Gly
        255                 260                 265

gat ccg cga gtt agg ccc acc ttc caa gaa att act tct gaa acc gag      868
Asp Pro Arg Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu
    270                 275                 280

gac ctg tgt gaa aag cct gat gac gaa gtg aaa gaa act gct cat gat      916
Asp Leu Cys Glu Lys Pro Asp Asp Glu Val Lys Glu Thr Ala His Asp
285                 290                 295                 300

ctg gac gtg aaa agc ccc ccg gag ccc agg agc gag gtg gtg cct gcg      964
Leu Asp Val Lys Ser Pro Pro Glu Pro Arg Ser Glu Val Val Pro Ala
                305                 310                 315

agg ctc aag cgg gcc tct gcc ccc acc ttc gat aac gac tac agc ctc     1012
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ggc ccc gag gag ctc agc cgc agc tcc tct gag tcc aag ctg cca tcg     1108
Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys Leu Pro Ser

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tcc ggc agt ggg aag agg ctc tcg ggg gtg tcc tcg gtg gac tcc gcc     1156
Ser Gly Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala
365                 370                 375                 380


ttc tct tcc aga gga tca ctg tcg ctg tcc ttt gag cgg gaa cct tca     1204
Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Pro Ser
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acc agc gat ctg ggt acc aca aga cgt cca gaa gaa gaa gct tgt gga     1252
Thr Ser Asp Leu Gly Thr Thr Arg Arg Pro Glu Glu Glu Ala Cys Gly
            400                 405                 410

tgc cat cgt gtc cgg gac acc agc aaa ctg atg aag atc ctg cag ccg     1300
Cys His Arg Val Arg Asp Thr Ser Lys Leu Met Lys Ile Leu Gln Pro
        415                 420                 425

cag gac gtg gac ctg gca ctg gac agc ggt gcc agc ctg ctg cac ctg     1348
Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu Leu His Leu
    430                 435                 440

gcg gtg gag gcc ggg caa gag gag tgc gcc aag tgg ctg ctg ctc aac     1396
Ala Val Glu Ala Gly Gln Glu Glu Cys Ala Lys Trp Leu Leu Leu Asn
445                 450                 455                 460

aat gcc aac ccc aac ctg agc aac cgt agg ggc tcc acc ccg ttg cac     1444
Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr Pro Leu His
                465                 470                 475

atg gcc gtg gag agg agg gtg cgg ggt gtc gtg gag ctc ctg ctg gca     1492
Met Ala Val Glu Arg Arg Val Arg Gly Val Val Glu Leu Leu Leu Ala
            480                 485                 490

cgg aag atc agt gtc aac gcc aag gat gag gac cag tgg aca gcc ctc     1540
Arg Lys Ile Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu
        495                 500                 505

cac ttt gca gcc cag aac ggg gat gag tct agc aca cgg ctg ctg ttg     1588
His Phe Ala Ala Gln Asn Gly Asp Glu Ser Ser Thr Arg Leu Leu Leu
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gag aag aac gcc tcg gtc aac gag gtg gac ttt gag ggc cgg acg ccc     1636
Glu Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro
525                 530                 535                 540

atg cac gtg gcc tgc cag cac ggg cag gag aat atc gtg cgc atc ctg     1684
Met His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Ile Leu
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ctg cgc cga ggc gtg gac gtg agc ctg cag ggc aag gat gcc tgg ctg     1732
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Leu Arg Arg Gly Val Asp Val Ser Leu Gln Gly Lys Asp Ala Trp Leu
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cca ctg cac tac gct gcc tgg cag ggc cac ctg ccc atc gtc aag ctg     1780
Pro Leu His Tyr Ala Ala Trp Gln Gly His Leu Pro Ile Val Lys Leu
        575                 580                 585

ctg gcc aag cag ccg ggg gtg agt gtg aac gcc cag acg ctg gat ggg     1828
Leu Ala Lys Gln Pro Gly Val Ser Val Asn Ala Gln Thr Leu Asp Gly
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agg acg cca ttg cac ctg gcc gca cag cgc ggg cac tac cgc gtg gcc     1876
Arg Thr Pro Leu His Leu Ala Ala Gln Arg Gly His Tyr Arg Val Ala
605                 610                 615                 620

cgc atc ctc atc gac ctg tgc tcc gac gtc aac gtc tgc agc ctg ctg     1924
Arg Ile Leu Ile Asp Leu Cys Ser Asp Val Asn Val Cys Ser Leu Leu
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gca cag aca ccc ctg cac gtg gcc gcg gag acg ggg cac acg agc act     1972
Ala Gln Thr Pro Leu His Val Ala Ala Glu Thr Gly His Thr Ser Thr
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gcc agg ctg ctc ctg cat cgg ggc gct ggc aag gag gcc gtg acc tca     2020
Ala Arg Leu Leu Leu His Arg Gly Ala Gly Lys Glu Ala Val Thr Ser
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gac ggc tac acc gct ctg cac ctg gct gcc cgc aac gga cac ctg gcc     2068
Asp Gly Tyr Thr Ala Leu His Leu Ala Ala Arg Asn Gly His Leu Ala
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act gtc aag ctg ctt gtc gag gag aag gcc gat gtg ctg gcc cgg gga     2116
Thr Val Lys Leu Leu Val Glu Glu Lys Ala Asp Val Leu Ala Arg Gly
685                 690                 695                 700

ccc ctg aac cag acg gcg ctg cac ctg gct gcc gcc cac ggg cac tcg     2164
Pro Leu Asn Gln Thr Ala Leu His Leu Ala Ala Ala His Gly His Ser
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gag gtg gtg gag gag ttg gtc agc gcc gat gtc att gac ctg ttc gac     2212
Glu Val Val Glu Glu Leu Val Ser Ala Asp Val Ile Asp Leu Phe Asp
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gag cag ggg ctc agc gcg ctg cac ctg gcc gcc cag ggc cgg cac gca     2260
Glu Gln Gly Leu Ser Ala Leu His Leu Ala Ala Gln Gly Arg His Ala
        735                 740                 745

cag acg gtg gag act ctg ctc agg cat ggg gcc cac atc aac ctg cag     2308
Gln Thr Val Glu Thr Leu Leu Arg His Gly Ala His Ile Asn Leu Gln
    750                 755                 760

agc ctc aag ttc cag ggc ggc cat ggc ccc gcc gcc aca ctc ctg cgg     2356
Ser Leu Lys Phe Gln Gly Gly His Gly Pro Ala Ala Thr Leu Leu Arg
765                 770                 775                 780

cga agc aag acc tag ctggctgcct gcggagaccg ggggtccacg tggggctctt     2411
Arg Ser Lys Thr  *

gtcctgtcct gtgttcctcg tggggatgga acgatcctgc gtggggcccc gttgtggctt   2471
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Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp Leu
        35                  40                  45
Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg Met
    50                  55                  60
Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg Tyr
65                  70                  75                  80
Ile Leu Pro Val Tyr Gly Ile Cys Arg Glu Pro Val Gly Leu Val Met
                85                  90                  95
Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu Pro
            100                 105                 110
Leu Pro Trp Asp Leu Arg Phe Arg Ile Ile His Glu Thr Ala Val Gly
        115                 120                 125
Met Asn Phe Leu His Cys Met Ala Pro Pro Leu Leu His Leu Asp Leu
    130                 135                 140
Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile Ser
145                 150                 155                 160
Asp Phe Gly Leu Ala Lys Cys Asn Gly Leu Ser His Ser His Asp Leu
                165                 170                 175
Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu Arg
            180                 185                 190
Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr Ser
        195                 200                 205
Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe Ala
    210                 215                 220
Asp Glu Lys Asn Ile Leu His Ile Met Val Lys Val Val Lys Gly His
225                 230                 235                 240
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Arg Pro Glu Leu Pro Pro Val Cys Arg Ala Arg Pro Arg Ala Cys Ser
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His Leu Ile Arg Leu Met Gln Arg Cys Trp Gln Gly Asp Pro Arg Val
            260                 265                 270
Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys Glu
        275                 280                 285
Lys Pro Asp Asp Glu Val Lys Glu Thr Ala His Asp Leu Asp Val Lys
    290                 295                 300
Ser Pro Pro Glu Pro Arg Ser Glu Val Val Pro Ala Arg Leu Lys Arg
305                 310                 315                 320
Ala Ser Ala Pro Thr Phe Asp Asn Asp Tyr Ser Leu Ser Glu Leu Leu
                325                 330                 335
Ser Gln Leu Asp Ser Gly Val Ser Gln Ala Val Glu Gly Pro Glu Glu
            340                 345                 350
Leu Ser Arg Ser Ser Ser Glu Ser Lys Leu Pro Ser Ser Gly Ser Gly
        355                 360                 365
Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala Phe Ser Ser Arg
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Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Pro Ser Thr Ser Asp Leu
385                 390                 395                 400
Gly Thr Thr Arg Arg Pro Glu Glu Glu Ala Cys Gly Cys His Arg Val
                405                 410                 415
Arg Asp Thr Ser Lys Leu Met Lys Ile Leu Gln Pro Gln Asp Val Asp
            420                 425                 430
Leu Ala Leu Asp Ser Gly Ala Ser Leu Leu His Leu Ala Val Glu Ala
        435                 440                 445
Gly Gln Glu Glu Cys Ala Lys Trp Leu Leu Leu Asn Asn Ala Asn Pro
    450                 455                 460
Asn Leu Ser Asn Arg Arg Gly Ser Thr Pro Leu His Met Ala Val Glu
465                 470                 475                 480
Arg Arg Val Arg Gly Val Val Glu Leu Leu Leu Ala Arg Lys Ile Ser
                485                 490                 495
Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His Phe Ala Ala
            500                 505                 510
Gln Asn Gly Asp Glu Ser Ser Thr Arg Leu Leu Leu Glu Lys Asn Ala
        515                 520                 525
Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met His Val Ala
    530                 535                 540
Cys Gln His Gly Gln Glu Asn Ile Val Arg Ile Leu Leu Arg Arg Gly
545                 550                 555                 560
Val Asp Val Ser Leu Gln Gly Lys Asp Ala Trp Leu Pro Leu His Tyr
                565                 570                 575
Ala Ala Trp Gln Gly His Leu Pro Ile Val Lys Leu Leu Ala Lys Gln
            580                 585                 590
Pro Gly Val Ser Val Asn Ala Gln Thr Leu Asp Gly Arg Thr Pro Leu
        595                 600                 605
His Leu Ala Ala Gln Arg Gly His Tyr Arg Val Ala Arg Ile Leu Ile
    610                 615                 620
Asp Leu Cys Ser Asp Val Asn Val Cys Ser Leu Leu Ala Gln Thr Pro
625                 630                 635                 640
Leu His Val Ala Ala Glu Thr Gly His Thr Ser Thr Ala Arg Leu Leu
                645                 650                 655
Leu His Arg Gly Ala Gly Lys Glu Ala Val Thr Ser Asp Gly Tyr Thr
            660                 665                 670
Ala Leu His Leu Ala Ala Arg Asn Gly His Leu Ala Thr Val Lys Leu
        675                 680                 685
Leu Val Glu Glu Lys Ala Asp Val Leu Ala Arg Gly Pro Leu Asn Gln
    690                 695                 700
Thr Ala Leu His Leu Ala Ala Ala His Gly His Ser Glu Val Val Glu
705                 710                 715                 720
Glu Leu Val Ser Ala Asp Val Ile Asp Leu Phe Asp Glu Gln Gly Leu
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                725                 730                 735
Ser Ala Leu His Leu Ala Ala Gln Gly Arg His Ala Gln Thr Val Glu
            740                 745                 750
Thr Leu Leu Arg His Gly Ala His Ile Asn Leu Gln Ser Leu Lys Phe
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Gln Gly Gly His Gly Pro Ala Ala Thr Leu Leu Arg Arg Ser Lys Thr
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Lys Glu Ser Leu Ser Leu Arg Glu Ile Gln Ile Leu Lys Arg Leu Ser
        35   40   45
His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Asp Thr Asp Asp
    50   55   60
His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp Leu Phe Asp
65   70   75   80
Tyr Leu Arg Arg Asn Gly Pro Leu Ser Glu Lys Glu Ala Lys Lys Ile
                85   90   95
Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Asn Gly Ile
            100   105   110
Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu Asn Gly
        115   120   125
Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Leu Glu Lys Leu
    130   135   140
Thr Thr Phe Val Gly Thr Pro Trp Tyr Met Met Ala Pro Glu Val Ile
145   150   155   160
Leu Glu Gly Arg Gly Tyr Ser Ser Lys Val Asp Val Trp Ser Leu Gly
                165   170   175
Val Ile Leu Tyr Glu Leu Leu Thr Gly Gly Pro Leu Phe Pro Gly Ala
            180   185   190
Asp Leu Pro Ala Phe Thr Gly Gly Asp Glu Val Asp Gln Leu Ile Ile
        195   200   205
Phe Val Leu Lys Leu Pro Phe Ser Asp Glu Leu Pro Lys Thr Arg Ile
    210   215   220
Asp Pro Leu Glu Glu Leu Phe Arg Ile Lys Lys Arg Arg Leu Pro Leu
225   230   235   240
Pro Ser Asn Cys Ser Glu Glu Leu Lys Asp Leu Leu Lys Lys Cys Leu
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<221> VARIANT
<222> 3, 5
<223> The Xaa at positions 3 and 5 can be any amino acid
      residue except Pro.

<220>

<221> VARIANT
<222> 6
<223> The Xaa at position 6 can be Phe, Tyr, Trp, Met, Gly, Ser, Thr, Asn, or His.

<220>
<221> VARIANT
<222> 7
<223> The Xaa at position 7 can be Ser, Gly or Ala.

<220>
<221> VARIANT
<222> 8
<223> The Xaa at position 8 can be any amino acid except Pro or Trp.

<220>
<221> VARIANT
<222> 9
<223> The Xaa at position 9 can be Leu, Ile, Val, Cys, Ala or Thr.

<220>
<221> VARIANT
<222> 10
<223> The Xaa at position 10 can be any amino acid except Pro or Asp.

<220>
<221> VARIANT
<222> 11
<223> The Xaa at position 11 can be any amino acid.

<220>
<221> VARIANT
<222> 12
<223> The Xaa at position 12 can be Gly, Ser, Thr, Ala, Cys, Leu, Ile, Val, Met, Phe or Tyr.

<220>
<221> VARIANT
<222> (13)...(30)
<223> The Xaa at positions 13 to 30 can be any amino acid.

<220>
<221> VARIANT
<222> (13)...(30)
<223> The number of Xaa residues in this portion of the consensus can vary between 5 residues and 18 residues.

<220>
<221> VARIANT
<222> 31
<223> The Xaa at position 31 can be Leu, Ile, Val, Met, Phe, Tyr, Trp, Cys, Ser, Thr, Ala, or Arg.

<220>
<221> VARIANT
<222> 32

<223> The Xaa at position 32 can be Ala, Ile, Val or
Pro.

<220>
<221> VARIANT
<222> 33
<223> The Xaa at position 33 can be Leu, Ile, Val, Met,
Phe, Ala, Gly, Cys, Lys, or Arg.

<400> 5
Xaa Gly Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Lys

<210> 6
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence for serine/threonine kinase active site

<220>
<221> VARIANT
<222> 1
<223> The Xaa at position 1 can be Leu, Ile, Val, Met,
Phe, Tyr or Cys.

<220>
<221> VARIANT
<222> 2,4,8,9
<223> The Xaa at positions 2, 4, 8 or 9 can be any amino
acid residue.

<220>
<221> VARIANT
<222> 3
<223> The amino acid residue at position 3 can be His or
Tyr.

<220>
<221> VARIANT
<222> 6
<223> The amino acid residue at position 6 can be Leu,
Ile, Val, Met, Phe or Tyr.

<220>
<221> VARIANT
<222> 11,12,13
<223> The Xaa at positions 11, 12, or 13 can be Leu,
Ile, Val, Met, Phe, Tyr, Cys or Thr.

<400> 6
Xaa Xaa Xaa Xaa Asp Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa
1 5 10

<210> 7
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence for aspartyl protease active site

<220>
<221> VARIANT
<222> 1
<223> The Xaa at position 1 can be Leu, Ile, Val, Met,
Phe, Gly, Ala or Cys.

<220>
<221> VARIANT
<222> 2
<223> The Xaa at position 2 can be Leu, Ile, Val, Met,
Thr, Ala, Asp or Asn.

<220>
<221> VARIANT
<222> 3
<223> The Xaa at position 3 can be Leu, Ile, Val, Phe,
Ser or Ala.

<220>
<221> VARIANT
<222> 5
<223> The Xaa at position 5 can be Ser or Thr.

<220>
<221> VARIANT
<222> 7
<223> The Xaa at position 7 can be Ser, Thr, Ala or Val.

<220>
<221> VARIANT
<222> 8
<223> The Xaa at position 8 can be Ser, Thr, Ala, Pro,
Asp, Glu, Asn, or Gln.

<220>
<221> VARIANT
<222> 9, 11
<223> The Xaa at positions 9 and 11 can be any amino
acid residue.

<220>
<221> VARIANT
<222> 10
<223> The Xaa at position 10 can be Leu, Ile, Val, Met,
Phe, Ser Thr, Asn, or Cys.

<220>
<221> VARIANT
<222> 12
<223> The Xaa at position 12 can be Leu, Ile, Val, Met,
Phe, Gly, Thr or Ala.

<400> 7

Xaa Xaa Xaa Asp Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 8
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence for ankyrin domain

<400> 8
Asp Gly Arg Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Glu
1 5 10 15
Val Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Val Asn Ala Arg Asp
20 25 30
Lys

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 9
ggcacggaag atcagtgtca 20

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 10
cgaggcgttc ttctccaaca 20

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> probe

<400> 11
agggctgtcc actggtcctc atcctt 26

<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 12
gatgtggttg aattcatgga gggcgacggc gggacc 36

<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
gatgctggct ctagaggtct tgcttcgccg caggagtgt 39

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 14
tccgagttgc tgtcacagtt g 21

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 15
cgatgggagc ttgcattca 19

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> probe

<400> 16
tcccagactc ttgaaggccc cga 23

<210> 17
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 17
Gln Ser Leu Lys Phe Gln Gly Gly His Gly Pro Ala Ala Thr Leu Leu
1 5 10 15
Arg Arg Ser Lys Thr

20

<210> 18
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 18
Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys Leu Pro Ser
1 5 10 15
Ser Gly Ser Gly
20

<210> 19
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 19
Ser Glu Thr Glu Asp Leu Cys Glu Lys Pro Asp Asp Glu Val Lys Glu
1 5 10 15
Thr Ala His Asp
20

<210> 20
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<221> SITE
<222> 1
<223> A biotin is covalently attached to the residue at position 1.

<400> 20
Lys Lys Arg Phe Ser Phe Lys Lys Ser Phe Lys Leu Ser Gly Phe Ser
1 5 10 15
Phe Lys

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA target sequence

<400> 21
aagaacatcc tgcacatcat g 21

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA target sequence

<400> 22
aagaagatgg agatggccaa g 21

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA target sequence

<400> 23
aaccttcaac cagcgatctg g 21

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA sense strand, nucleotides 1-21 are ribonucleic acid, nucleotides 22 and 23 are deoxyribonucleic acid.

<400> 24
aagaacaucc ugcacaucau gtt 23

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA anti-sense strand, complement of SEQ ID NO:24, nucleotides 1-21 are ribonucleic acid, nucleotides 22-23 are deoxyribonucleic acid.

<400> 25
caugaugugc aggauguucu utt 23

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA sense strand, nucleotides 1-21 are ribonucleic acid, nucleotides 22 and 23 are deoxyribonucleic acid.

<400> 26
aagaagaugg agauggccaa gtt 23

<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA anti-sense strand, complement of SEQ ID NO:26, nucleotides 1-21 are ribonucleic acid, nucleotides 22 and 23 are deoxyribonucleic acid.

<400> 27
cuuggccauc uccaucuucu utt 23

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA sense strand, nucleotides 1-21 are ribonucleic acid, nucleotides 22 and 23 are deoxyribonucleic acid.

<400> 28
aaccuucaac cagcgaucug gtt 23

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA anti-sense strand, complement of SEQ ID NO:28, nucleotides 1-21 are ribonucleic acid, nucleotides 22 and 23 are deoxyribonucleic acid.

<400> 29
ccagaucgcu gguugaaggu utt 23